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Evaluation of two live, cold-passaged, temperature-sensitive respiratory syncytial virus vaccine: in chimpanzees and in human adults, infants, and children.

Karron RA, Wright PF, Crowe JE Jr, Clements-Mann ML, Thompson J, Makhene M, Casey R, Murphy BR.

Center for Immunization Research, Department of International Healt School of Hygiene and Public Health, The Johns Hopkins University, Baltimore, Maryland 21205, USA.

Two live-attenuated, cold-passaged (cp), temperature-sensitive (ts) candidate vaccines, designated cpts530/1009 and cpts248/955, were attenuated, genetically stable, and immunogenic in chimpanzees and were highly attenuated for human adults. In respiratory syncytial virus (RSV)-seropositive children, cpts530/1009 was more restricted in replication than cpts248/955. In seronegative children, 10(4) pfu of cpts248/955 was insufficiently attenuated, and a high titer of vaccine virus was shed (mean peak titer, 10(4.4) pfu/mL), whereas 10(4) pfu c cpts530/1009 was relatively attenuated and restricted in replication (mean peak titer, 10(2.0) pfu/mL). At a dose of 10(5) pfu, cpts530/1009 was immunogenic in seronegative children (geometric mean titer of RSV neutralizing antibodies, 1:724). Transmission of either vaccine to seronegative placebo recipients occurred at a frequency of 20%-25%. Of importance, vaccine viruses recovered fro chimpanzees and humans were ts. In contrast to previous studies, this study indicates that live attenuated RSV vaccines that are immunogen and phenotypically stable can be developed. Additional studies are

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1: J Infect Dis 2000 May;181(5):1547-56

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Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial viruses isolated over 9 consecutive epidemics in Korea.

Choi EH, Lee HJ.

Immunocompromised Host Section, Pediatric Oncology Branch, National Cancer Institute, National Institutes of Health, Bethesda, Maryland, USA.

To study genetic variation and molecular epidemiology of the G protein of respiratory syncytial virus (RSV), 253 strains from a children's hospital in Korea over 9 consecutive epidemics were analyzed. Restriction analysis of the entire G protein gene demonstrated 24 genotypes among 188 subgroup A and 6 among 65 subgroup B isolates. Two to 4 dominant genotypes of subgroup A cocirculated, and different genotypes predominated in each epidemic. Predominant genotypes were replaced with new genotypes during consecutive epidemics. One of 2 dominant genotypes among subgroup B predominated alternately or concurrently. Phylogenetic analysis revealed that there were multiple lineages, with clustering related to their location and time of isolation among strains from Korea and worldwide. Geographic and temporal distinction have been shown more clearly for subgroup B than subgroup A. These results suggest that the G protein of RSV is continuously evolving, with a distinct pattern presumably due to immune selection in a localized region over time.

PMID: 10823752 [PubMed - indexed for MEDLINE]

being conducted to identify a live RSV vaccine that is slightly more attenuated and less transmissible than cpts530/1009.

Publication Types:
- Clinical Trial
- Randomized Controlled Trial

PMID: 9395351 [PubMed - indexed for MEDLINE]

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